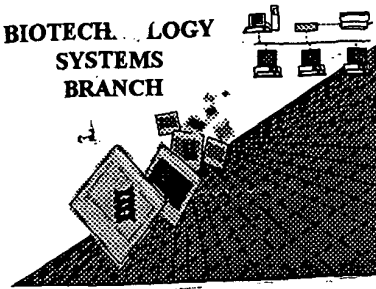


0570
0886

BIOTECH. LOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/721,904

Source: OIPK

Date Processed by STIC: 8/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/721,904

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/721,904

DATE: 08/07/2001

TIME: 13:33:47

Input Set : A:\seqlist.asc.txt

Output Set: N:\CRF3\08072001\I721904.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: JULIUS, Michael H.
 4 FILIPP, Dominik
 6 <120> TITLE OF INVENTION: THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY
 7 LAIT/sCD14-PROTEIN
 9 <130> FILE REFERENCE: 47841/00063
 11 <140> CURRENT APPLICATION NUMBER: US 09/721,904
 12 <141> CURRENT FILING DATE: 2000-11-27
 14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00482
 15 <151> PRIOR FILING DATE: 1999-05-27
 17 <150> PRIOR APPLICATION NUMBER: US 60/086,884
 18 <151> PRIOR FILING DATE: 1998-05-27
 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: Wordperfect 9.0

pp 1-3

ERRORED SEQUENCES

159 <210> SEQ ID NO: 4
 160 <211> LENGTH: 3738 (p. 2)
 161 <212> TYPE: PRI
 162 <213> ORGANISM: bovine
 164 <400> SEQUENCE: 4
 165 Met Val Cys Val Pro Tyr Leu Leu Leu Leu Leu Leu Pro Ser Leu Leu
 166 1 5 10 15
 168 Arg Val Ser Ala Asp Thr Thr Glu Pro Cys Glu Leu Asp Asp Asp Asp
 169 20 25 30
 171 Phe Arg Cys Val Cys Asn Phe Thr Asp Pro Lys Pro Asp Trp Ser Ser
 172 35 40 45
 174 Ala Val Gln Cys Met Val Ala Val Glu Val Glu Ile Ser Ala Gly Gly
 175 50 55 60
 177 Arg Ser Leu Glu Gln Phe Leu Lys Gly Ala Asp Thr Asn Pro Lys Gln
 178 65 70 75 80
 180 Tyr Ala Asp Thr Ile Lys Ala Leu Arg Val Arg Arg Leu Lys Leu Gly
 181 85 90 95
 183 Ala Ala Gln Val Pro Ala Gln Leu Leu Val Ala Val Leu Arg Ala Leu
 184 100 105 110
 186 Gly Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Glu Val Thr
 187 115 120 125
 189 Gly Pro Thr Pro Pro Thr Pro Leu Glu Ala Ala Gly Pro Ala Leu Thr
 190 130 135 140
 192 Thr Leu Ser Leu Arg Asn Val Ser Trp Thr Thr Gly Gly Ala Trp Leu
 193 145 150 155 160
 195 Gly Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Arg Val Leu Asn Ile
 196 165 170 175
 198 Ala Gln Ala His Ser Leu Ala Phe Pro Cys Ala Gly Leu Ser Thr Phe
 199 180 185 190
 201 Glu Ala Leu Thr Thr Leu Asp Leu Ser Asp Asn Pro Ser Leu Gly Asp

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/721,904

DATE: 08/07/2001

TIME: 13:33:47

Input Set : A:\seqlist.asc.txt

Output Set: N:\CRF3\08072001\I721904.raw

```

202          195          200          205
204 Thr Gly Leu Met Ala Ala Leu Cys Pro Asn Lys Phe Pro Ala Leu Gln
205          210          215          220
207 Tyr Leu Ala Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys
208 225          230          235          240
210 Ala Ala Leu Ala Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser
211          245          250          255
213 His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp
214          260          265          270
216 Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln
217          275          280          285
219 Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys
220          290          295          300
222 Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn
223 305          310          315          320
225 Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln
226          325          330          335
228 His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg
229          340          345          350
231 Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly
232          355          360          365
234 Ala Arg Gly Phe Ala
E--> 235          370
393 <210> SEQ ID NO: 7
394 <211> LENGTH: 377
395 <212> TYPE: PRT
396 <213> ORGANISM: rabbit
398 <400> SEQUENCE: 7
E--> 399 Met Glu Pro Val Pro Cys Leu Leu Leu Leu Leu Leu Pro Xaa Leu Leu
400 1          5          10          15
402 Arg Ala Ser Thr Asp Thr Pro Glu Pro Cys Glu Leu Asp Asp Asp Asp
403          20          25          30
405 Ile Arg Cys Val Cys Asn Phe Ser Asp Pro Gln Pro Asp Trp Ser Ser
406          35          40          45
408 Ala Leu Gln Cys Met Pro Ala Val Gln Val Glu Met Trp Gly Gly Gly
409          50          55          60
411 His Ser Leu Glu Gln Phe Leu Arg Gln Ala Asp Leu Tyr Thr Asp Gln
412 65          70          75          80
414 Arg Arg Tyr Ala Asp Val Val Lys Ala Leu Arg Val Arg Arg Leu Thr
415          85          90          95
417 Val Gly Ala Val Gln Val Pro Ala Pro Leu Leu Leu Gly Val Leu Arg
418          100          105          110
420 Val Leu Gly Tyr Ser Arg Leu Lys Glu Leu Ala Leu Glu Asp Ile Glu
421          115          120          125
423 Val Thr Gly Thr Ala Pro Pro Pro Pro Pro Leu Glu Ala Thr Gly Pro
424          130          135          140
426 Ala Leu Ser Thr Leu Ser Leu Arg Asn Val Ser Trp Pro Lys Gly Gly
427 145          150          155          160
429 Ala Trp Leu Ser Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Gln Val

```

see item 9 on
Errata
summary
sheet

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/721,904

DATE: 08/07/2001

TIME: 13:33:47

Input Set : A:\seqlist.asc.txt

Output Set: N:\CRF3\08072001\I721904.raw

430 165 170 175
 432 Leu Asn Ile Ala Gln Ala His Thr Leu Ala Phe Ser Cys Glu Gln Val
 433 180 185 190
 435 Arg Thr Phe Ser Ala Leu Thr Thr Leu Asp Leu Ser Glu Asn Pro Gly
 436 195 200 205
 438 Leu Gly Glu Arg Gly Leu Val Ala Ala Leu Cys Pro His Lys Glu Pro
 439 210 215 220
 441 Ala Leu Gln Asp Leu Ala Leu Arg Asn Ala Gly Met Lys Ile Leu Gln
 442 225 230 235 240
 444 Gly Val Cys Ala Ala Leu Ala Glu Ala Gly Val Gln Pro His His Leu
 445 245 250 255
 E--> 447 Asp Leu Ser His Asn Ser Leu Arg Xaa Xaa Xaa Ala Xaa Asp Thr Gln
 448 260 265 270
 450 Arg Cys Ile Trp Pro Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Thr
 451 275 280 285
 453 Gly Leu Gln Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Asn Val Leu
 454 290 295 300
 456 Asp Leu Ser Cys Asn Lys Leu Asn Arg Ala Pro Gln Pro Gly Glu Leu
 457 305 310 315 320
 459 Pro Lys Val Val Asn Leu Ser Leu Asp Gly Asn Pro Phe Leu Val Pro
 460 325 330 335
 462 Gly Ala Ser Lys Leu Gln Glu Asp Leu Thr Asn Ser Gly Val Phe Pro
 463 340 345 350
 465 Ala Cys Pro Pro Ser Pro Leu Ala Met Gly Met Ser Gly Thr Leu Ala
 466 355 360 365
 468 Leu Leu Gln Gly Ala Arg Gly Phe Ile
 469 370 375

9
 Lem 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/721,904

DATE: 08/07/2001

TIME: 13:33:48

Input Set : A:\seqlist.asc.txt

Output Set: N:\CRF3\08072001\I721904.raw

L:120 M:112 C: (48) String data converted to lower case,

M:112 Repeated in SeqNo=3

L:235 M:252 E: No. of Seq. differs, <211>LENGTH:Input:3738 Found:373 SEQ:4

L:399 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7

M:340 Repeated in SeqNo=7